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SASPKRRKKEEVVVGPVAGQARPGLQQVGNVVEGMQVGVGCQVGVGTMPLGDQLLV 281
                 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scharte J., Baur B.;
"A stress induced transcription factor of the AP2 gene family from the inducible CAM plant Mesembryanthemum crystallinum L.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR245119; AAF63205.1; ...
Interpro; IPR001471; AP2-domain.
Pfam; PF00087; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom: PD001423; AP2-domain; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PESFAAVDSVPVK-KEKTSPVSAAVTAAKGKHYRGVRQRPWGKFAAEIRDPAKNGARVWL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQSIKPVYGRNPSFSKLYPCFTESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSD 103
                                                                                                                                                                                 EDRSSFPSVKIETPESFAAVDSVPVKKEKTSPVSAAVTAAKGKHYRGVRQRPWGKFAAEI 163
                                                                                                                                                                                                                       EDRSSFPSVKIETPESFAAVDSVPVKKEKTSPVSAAVTAAKGKHYRGVRQRPWGKFAAEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesembryanthemum crystallinum (Common ice plant).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                     RDPAKNCARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GGMDKGLTVKCEVVEVARGDRLLV 267
                                                         ;
0
                 Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.0%; Score 731; DB 10; Length 282; 55.4%; Pred. No. 8e-57; Live 36; Mismatches 52; Indels 44
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                 224 SFSSSNENGAPKKRRTVAAGGGMDKGLTVKCEVVEVARGDRLLVL 268
                                                                                                                                                                                                                                                                                                                                                                    181 SFSSNENGAPKKRRTYVAAGGGMDKGLTVKCEVVEVARGDRLLVL 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AP2-RELATED TRANSCRIPTION FACTOR.
Score 1169; DB 10;
Pred. No. 1e-95;
---nhes 0;
84.8%; Scor. 100.0%; Pred. No. 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=LEAF;
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Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.; "Characterization of gene expression of NSERFs, transcription factors of basic PR genes from Nicotiana sylvestris."; Plant Call Physiol. 41:817-924(2000).
EMBL; ABO16264; BAA91122.1; ...
InterPro; IPR001471; AP2-domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 PVYGRNPSFSKLYPCFTESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSDEDRSS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 FPSVKIETPESFAAVDSVPVKKEKTSPVSAAVTAAKGKHYRGVRQRPWGKFAAEIRDPAK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PVYHRTSSFSSLMPCLTDTWGDLPLKVDDSEDMVIYGLLSDALTTGWTPFNLTSTEIKAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 NGARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                      Nicotiana sylvestris (Wood tobacco).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheog Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

NCBI_TaxID=4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 -SSFSSSNENGAPKKRRTVAAG-----GGMDKGLTVKCEVVEVARGDRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01BC3EEB51E46298 CRC64;
                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
42.7%; Score 589; DB 10;
Best Local Similarity 51.5%; Pred. No. 2.3e-44;
Matches 120; Conservative 31; Mismatches 62;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                 Created)
PRT;
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STRAIN-BY4; TISSUE=LEAF;
MEDLINE=95276459; PubMed=7756828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00847; AP2-domain; 1.
PRINKY: PR00367; ETHRSPELEMNT.
ProDom; PD001423; AP2-domain; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26243 MW;
                                              (TrEMBLrel. 15, (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AA;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 PubMed=10945353;
                                              01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q40479;
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                       Q9LW50;
09LW50
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C.R.,

Σ.

B., Miranda

us-09-533-029-18.rspt

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RESULT 082447

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EREBP ISOLOG (PUTATIVE ETHYLENE RESPONSE ELEMENT BINDING PROTEIN).
T13E15.15 OR AT2G44840.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 VYGRNPSFSKLYPCFTESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSDEDRSSF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 MYFRNPSFSNV--ILNDNWSDLPLSVDDSQDMAIYNTLRDAVSSGWTP-----SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSVKIETPESFAAVDSVPVKKEKTSPVSAAVTAA---KGKHYRGVRQRPWGKFAAEIRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
BINDING PROTEINI HOMOLOG (FRAGMENT).
                                                                                                                                                                                              Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D., Somerville
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Ashida Y., Hirata T.;
"ethylene-responsive element binding proteinl (EREBP) homolog,
Matricaria chamomilla.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Mira Palm C.J., Theologis A., Ecker J., Davis R.W.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002388; AAC31840.1; -.
EMBL; AF325089; AAK17157.1; -.
HSSP; O80337; 2GCC.
InterPro; IPR001471; AP2-domain.
InterPro; IPR001977; DNA_11gase.
                                                                                                                                                                                                                                                      Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00697; DNA_LIGASE_A1; UNKNOWN_1.
226 AA; 25353 MW; 4B2EF81CDD856987 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.7%; Score 423.5; DB 10; Best Local Similarity 47.2%; Pred. No. 9.7e-30; Matches 92; Conservative 28; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; AP2-domain; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, ETHYLENE-RESPONSIVE ELEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00847; AP2-domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 FSSSNENGAPKKRRT 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matricaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matricaria chamomilla.
Eukaryota; Viridiplant
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=98504;
                                                                                            eurosids II; Bra
NCBL_TaxID=3702;
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Anthemideae,
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 169 NGARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKRSSF--- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSDEDRSSFPSVKIETPESFAAVDS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 VPVKKEKTSPVSAAVTAAKGKHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFETAEDAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 LAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKRSSF---SSSNENGAPKKRRTVAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.

NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNU-2001 (TrEMBLrel.), Last annotation update)
ETHYLENE RESPONSE ELEMENT BINDING PROTEIN 1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22616 MW; F62AB477B0B017DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tobacco genes.";
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Last annotation update)
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| 86 ASSSENSSPKRRKAVA-----TEKSEAVEVESKSNVL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%; Score 476; DB 10;
llarity 47.9%; Pred. No. 1.9e-34;
Conservative 37; Mismatches 50;
                                                                                                                                   226 SSSNENGAPKKRRTVAAGGGMDKGLTVKCEVVEVARGDRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. BRIGHT YELLOW 2;
MEDLINE-9883243; PubMed=9725022;
MEDLINE-9883243; PubMed=9725022;
MEDLINE-9883243; PubMed=9725022;
Frour classes of salicylate-induced tobacco ge Mol. Plant Microbe Interact. 11:895-905(1998).
MSPP; 080337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AA.
                                                                                                                                                                                                                                                                      203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AEKSGAVEVESKSNVLQVGCQVELLTRGHQLLV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 ---GGGMD----KGLTVKCEVVEVARGDRLLV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR001471; AP2-domain.
Pfam; PF00847; AP2-domain; 1.
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ProDom; PD001423; AP2-domain; 1
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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MW; 13E7ED8C819D5F48 CRC64;

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32878
 SMART; SM00380; AP2; 1. SEQUENCE 291 AA; 328
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                                                                                                                       Ritajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
"Characterization of gene expression of NSERFS, transcription factors of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-24(2000).
EMBL; AB016266; BAA97124.1;
EMBL; AB016266; BAA97124.1;
Enterpro; IRR001471; AP2-domain.
Proms; PR00187; AP2-domain.
Probom; PD001423; AP2-domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                           60 LYPCFTESWGDLPLKE--NDSEDMLVYGILNDAFHGGWEPSSS---SSDEDRSSF----P 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 SVKIETPESFAAVDSVPVKKEKTSPVSAAVTAAKGKHYRGVRQRPWGKFAAEIRDPAKNG 170
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                           5 ADSQSDYAFLESIRRHLLGES---EPILSESTASSV--TQSCVTGQSIKPVYGRNPSFSK, 59
                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                         2 ASPQENSTILDLIRQHLLDDNVFLEHYCSETETTILIXSQSSSSSESLDQSFSFEPTLN-
                                                                                                                                                                                                                                                                                                                                                                                                           | :| :| :| :|| 61 -YATTAQS-SNLEVSTFFNNSKTEF-----DSFEFGTIPNVSAARSSSLKQTSFKERKP
                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                                                                                                                                                                                                         24.1%; Score 331.5; DB 10; Length 282; 39.9%; Pred. No. 1.8e-21; Live 39; Mismatches 57; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins that interact with
                                                                                                                                                                                                                                       SMART; SM00380; AP2; 1.
SEQUENCE 282 AA: 31831 MW; 8C6C62E72660D1C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 ARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 AA
ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BY4; TISSUE=LEAF;
MEDLINE=9226459; PubMed=7756828;
Ohme-Takagi M., Shinshi H.;
"Ethylene-inducible DNA binding profethylene-responsive element.";
Plant Cell 7:173-182(1995).
                        Nicotiana sylvestris (Wood tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana tabacum (Common tobacco)
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InterPro; IPR001471; AP2-domain.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; AP2-domain; 1.
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                                                                                                                                                                                                                                                                                    Lery Match
Sest Local Similarity 39.99
Watches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T02656;
                                                                                                                PubMed=10945353;
                                                                        NCBI_TaxID=4096;
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                                                                                                                                                                                                                                                                                                                              102 SDEDRSSF----PSVKIETP----ESFAAVDSVPVKKEKTSPVSAAVTAAKGKHYRGVRQ 153
                                                                                                                                                                                                                                                                                                                                                                                    106 NSPKQTSFKERKPSLNIAIPMKQQEVVQKVEVVPTEK-------KHYRGVRQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                              -----LKYADTAQSSNLDISSFFNNSKTEFDSFEFETKPNVSAARISS 105
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                                                                                                                                                                                                                     SFSKLYPCFTESWGDLPLKEND---SEDMLVYGILN-----DAFHGGWEPS----SSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van der Fits L., Memelink J.;
"ORCA3, a jasmonate-responsive transcriptional regulator of plant
primary and secondary metabolism.";
Science 289:295-297(2000).
EMBL; AJ251250, CAB96900.1; -.
EMBL; AJ251249; CAB96899.1; -.
                                                                                                                                                 2 ASPQENCTTLDLIRQHLLDDNVFMEHYCPQPILYSQSSSSESLNSIASELNNETFSFEP
                                                                                                                                                                                                                                                                                                                                                                                                                                          RPWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytbs; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Gentianales; Apocynaceae; Catharanthus. NCBI_TaxID=4058;
                                                        75;
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  Length 291;
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                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 DPVRIKSKRSSFSSSNENGAPKKRRTVAAGGGMDKGLTVKCEV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --ANFKOODNEILQPANSGRKRMRET-----ENEEIVIKKEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AP2-DOMAIN DNA-BINDING PROTEIN.
     DB 10;
23.9%; Score 329.5; DB 10; 32.9%; Pred. No. 2.8e-21; ive 43; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .69
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23.5%; Score 324; DB 10;
Best Local Similarity 36.0%; Pred. No. 5.4e-21;
Matches 91; Conservative 27; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=G.DON; TISSUE=ROOT; MEDLINE=20355201; PubMed=10894776;
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ProDom; PD001423; AP2-domain;
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Query Match 23.9
Best Local Similarity 32.9
Matches 93; Conservative
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178 FETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR------SSFS 226
                                                                               108 SFPSV-KIETPESFAAVDSVPVKKE-KTSPVSA-----AVTAAKGKHYRGVRQRPWGK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 FAAEIRDPAKNGARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Gaps
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Kannan P.;
"Genetic mapping of ripening and ethylene related loci in tomato.";
Theor. Appl. Genet. 98:1005-1013(1999).
RMBL, ARZ04784, AAG49031.1;
-InterPro; IPR001471, AP2-domain.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMWT.
PRINTS; PR00367; ETHRSPELEMWT.
SMART; SM0380; AP2, 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum (Tomato).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%; Score 318.5; DB 10; Length 214; 46.2%; Pred. No. 1.8e-20; tive 24; Mismatches 48; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 AA; 24102 MW; 45D8631266C1E085 CRC64;
                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIPENING REGULATED PROTEIN DDTFR10/A (FRAGMENT).
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Best Local Similarity 46.2%
Matches 73; Conservative
                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                          227 SSNEN-GAPKKRR 238
                                                                                                                                            190 SSSENSGGRKKRR 202
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